Figure 1

Figure 2

Figure 3
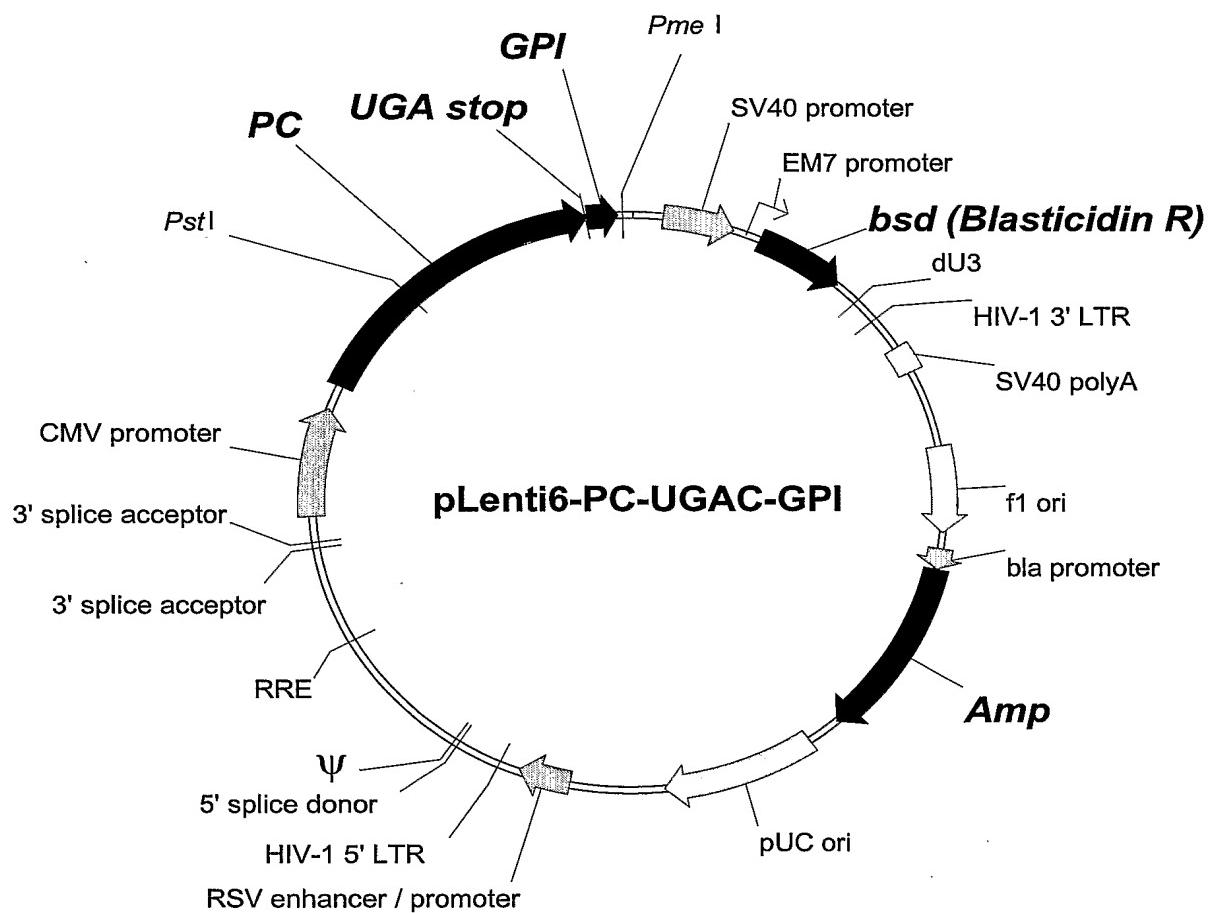
Figure 4
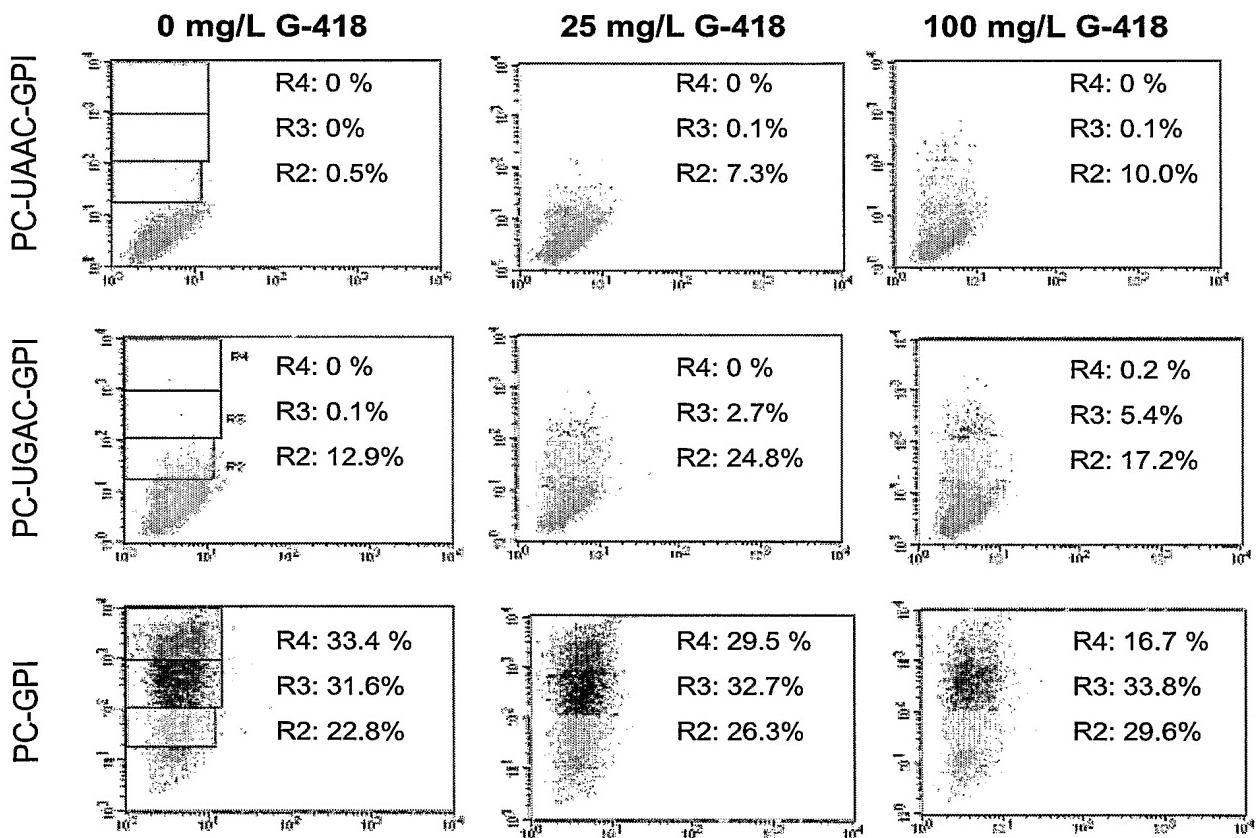
Figure 5
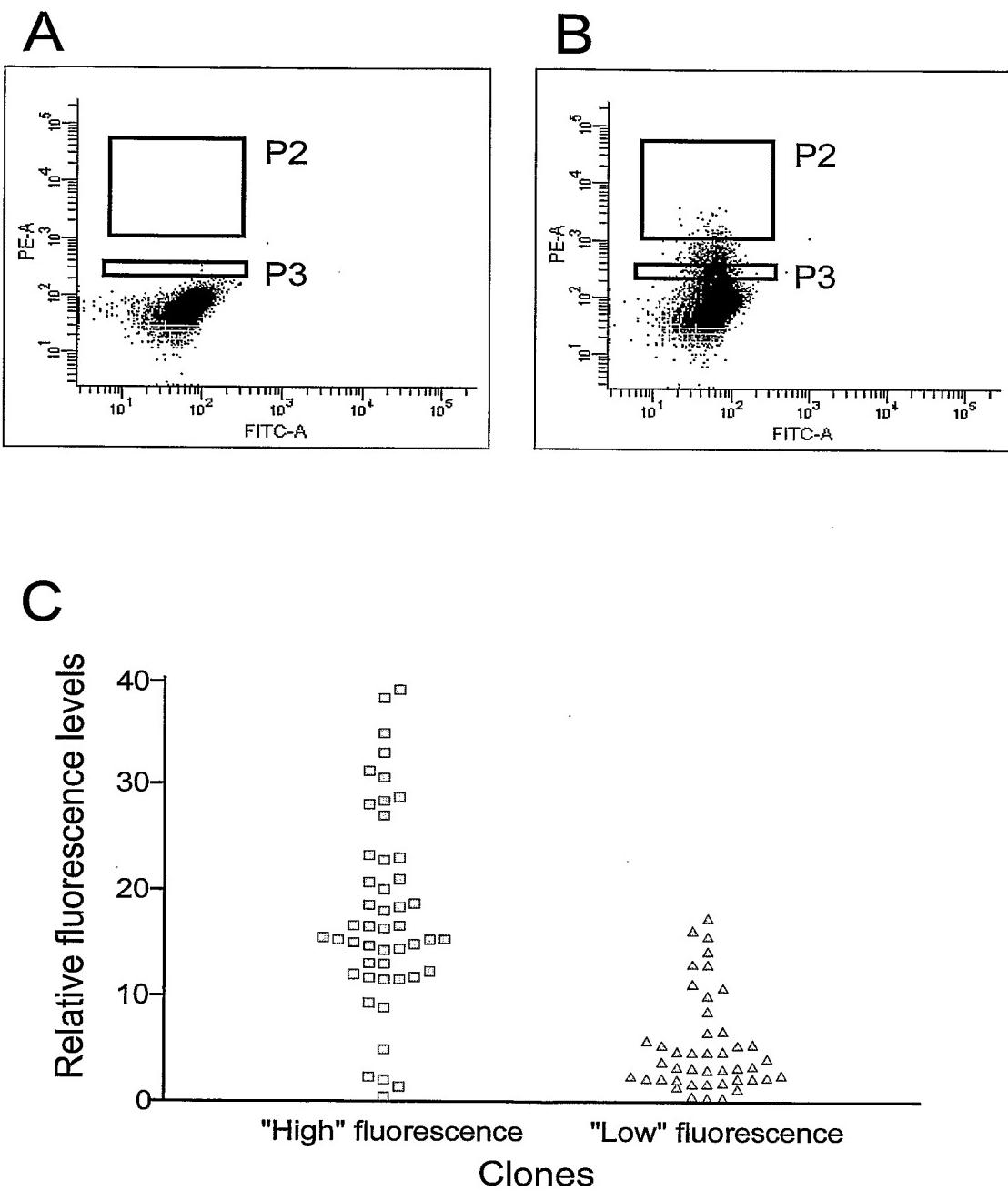
Figure 6

A
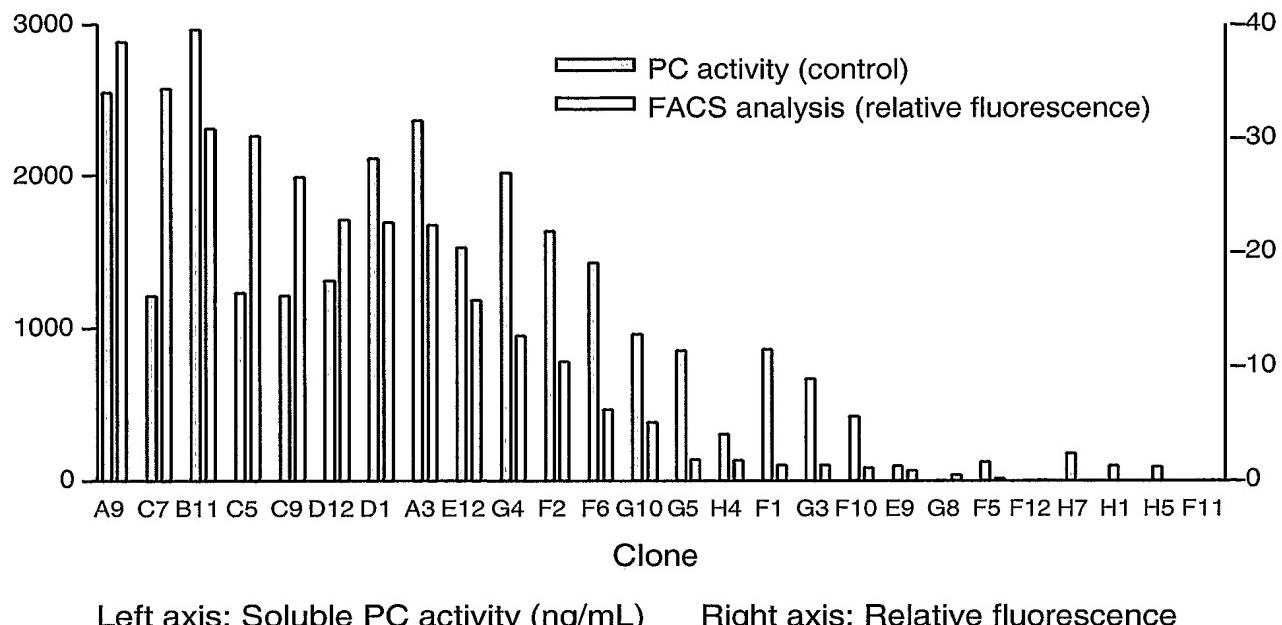
Left axis: Soluble PC activity (ng/mL)   Right axis: Relative fluorescence

B

Figure 7

Figure 8

Figure 9

pCDNA6-FVII-UAA-EGFPd

UAA stop

FVII

EGFPd

BGH poly-A

f1 ori

Intron
pCl-Neo

SV40 ori & pro

CMV pro

EM7 pro

bsd (blasticidin R)

bla pro

SV40 poly-A

Amp R

pUC ori
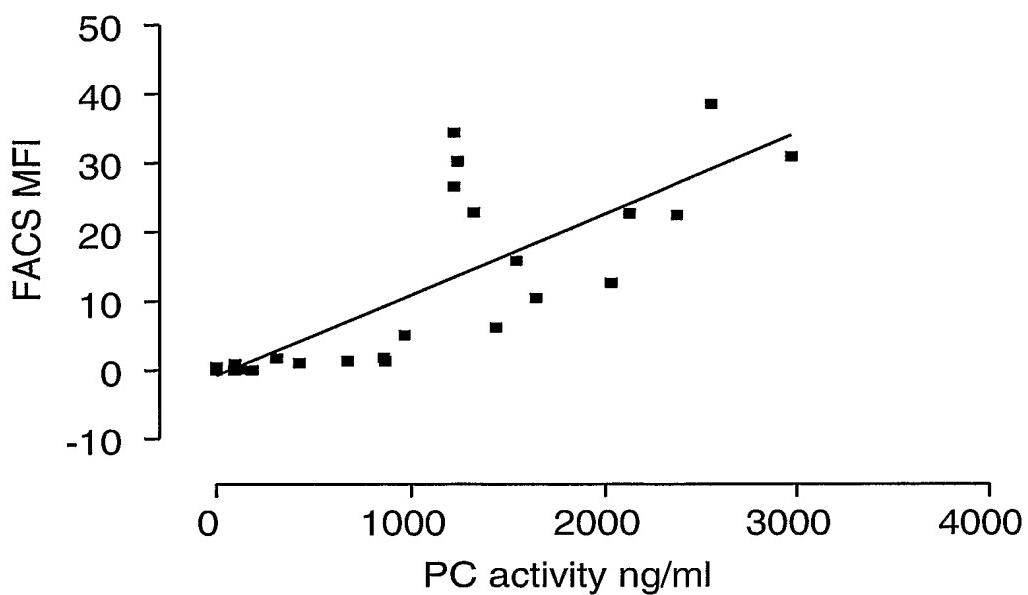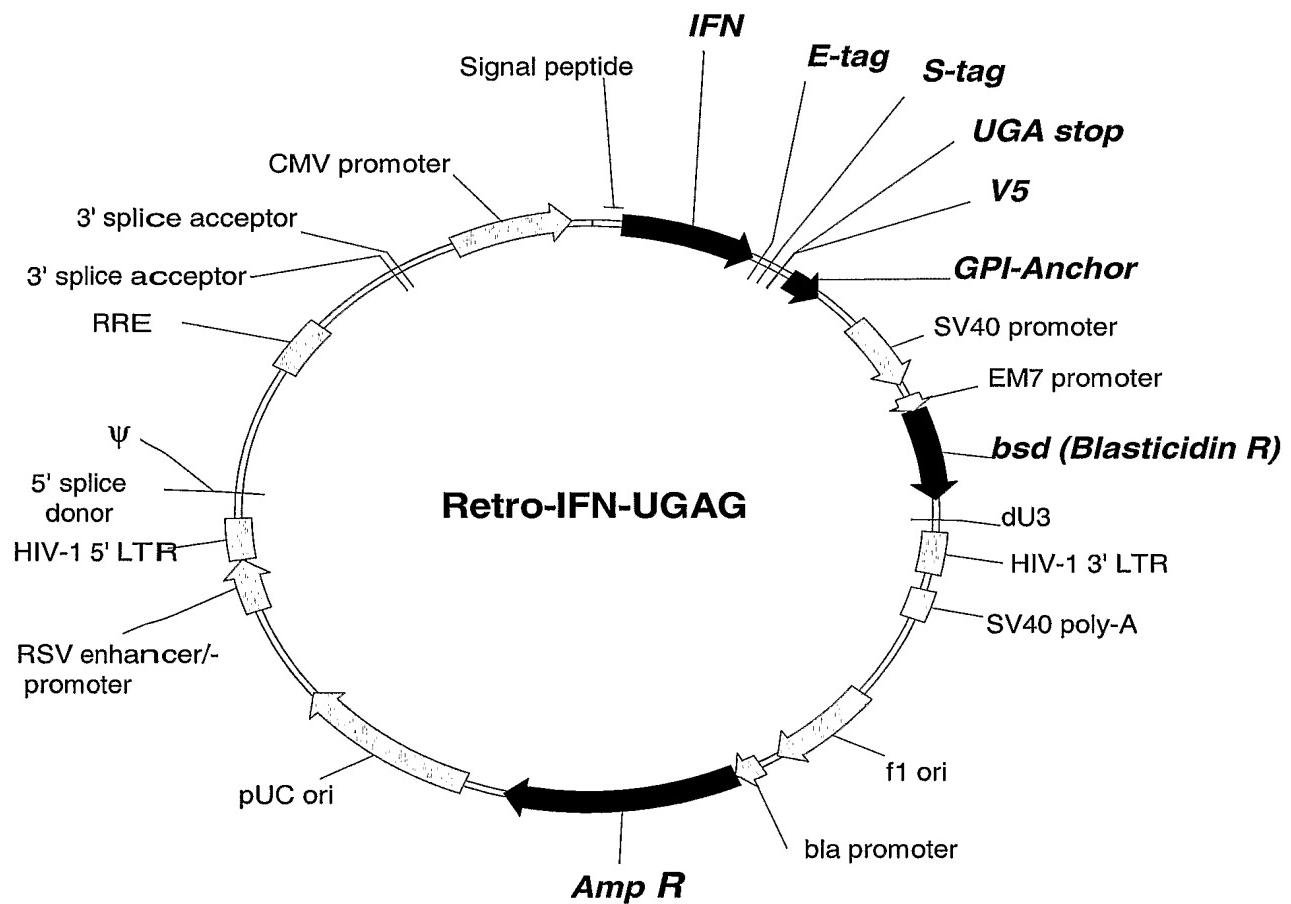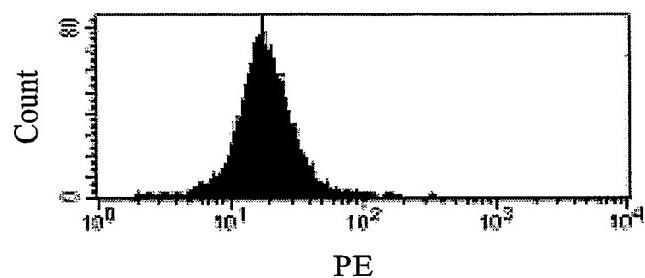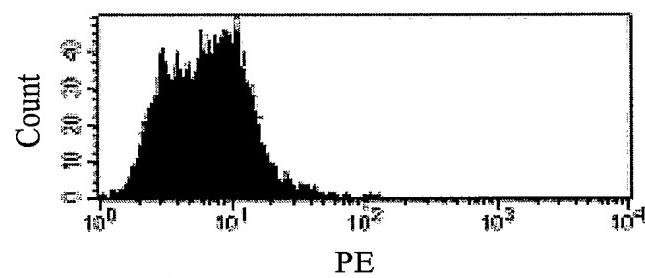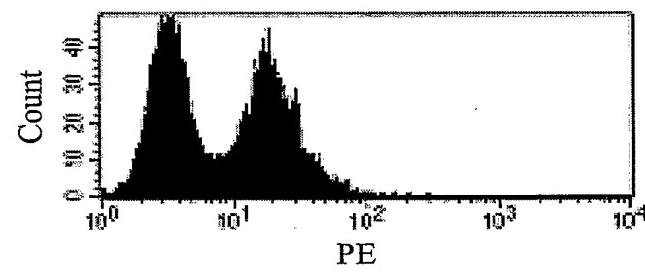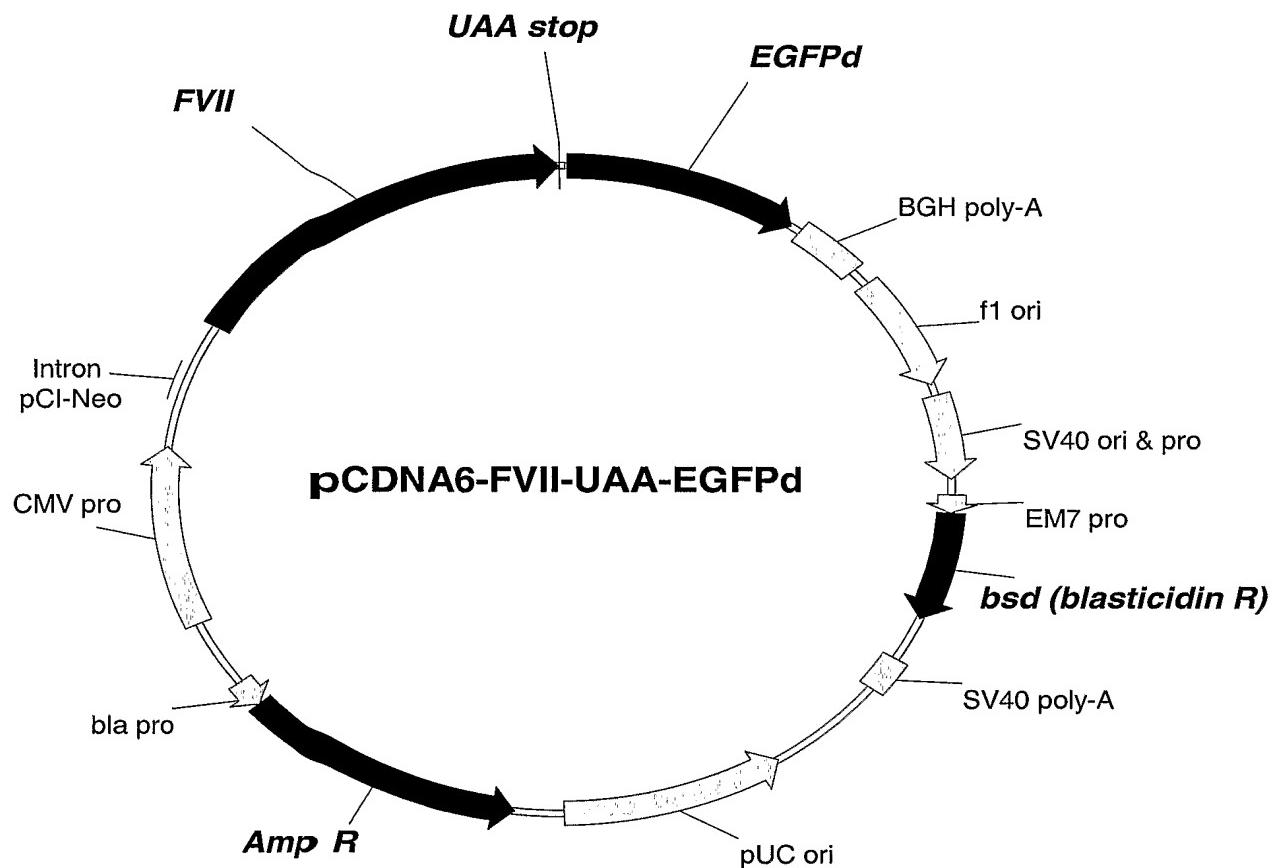
Figure 10

Figure 11

pCDNA6–FVII-UAA-GPI
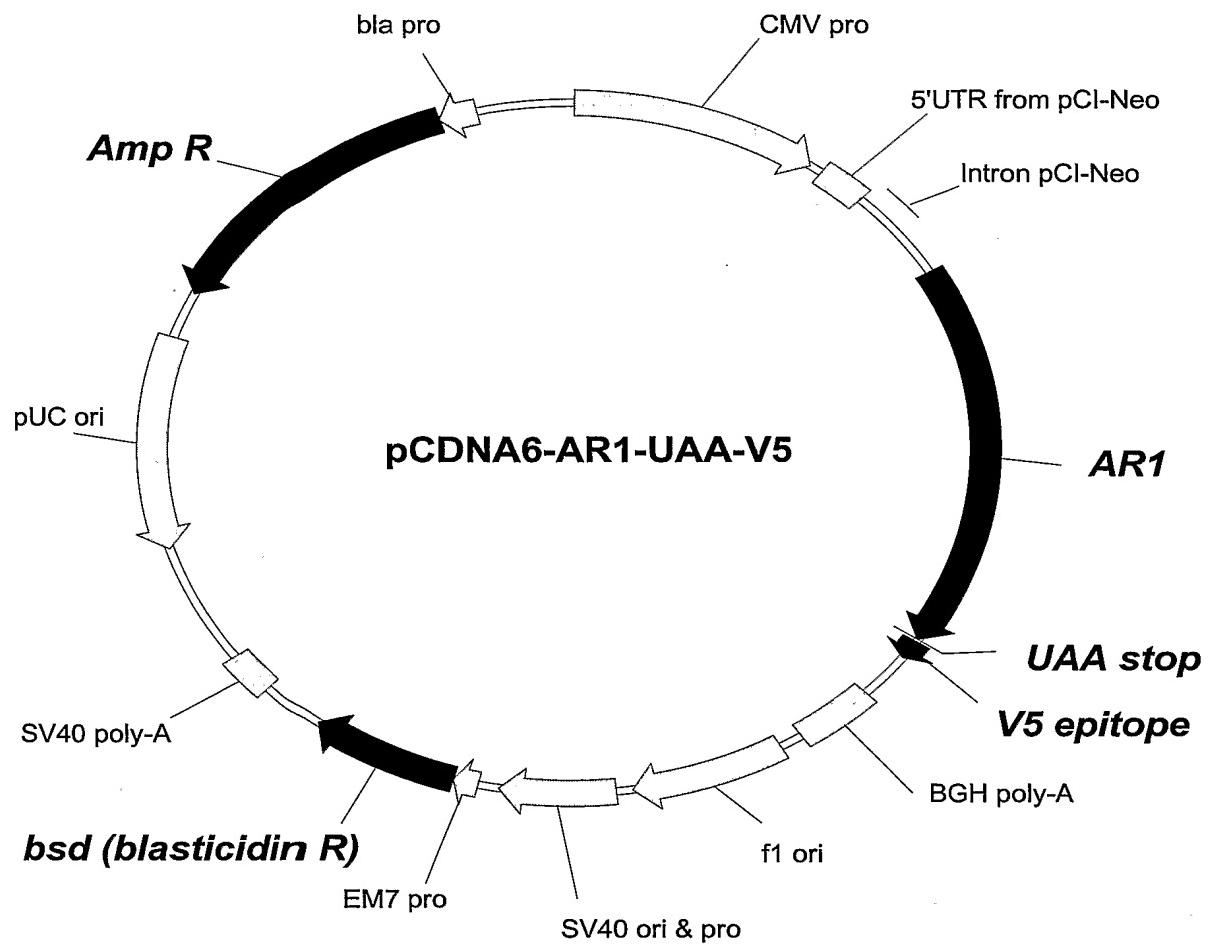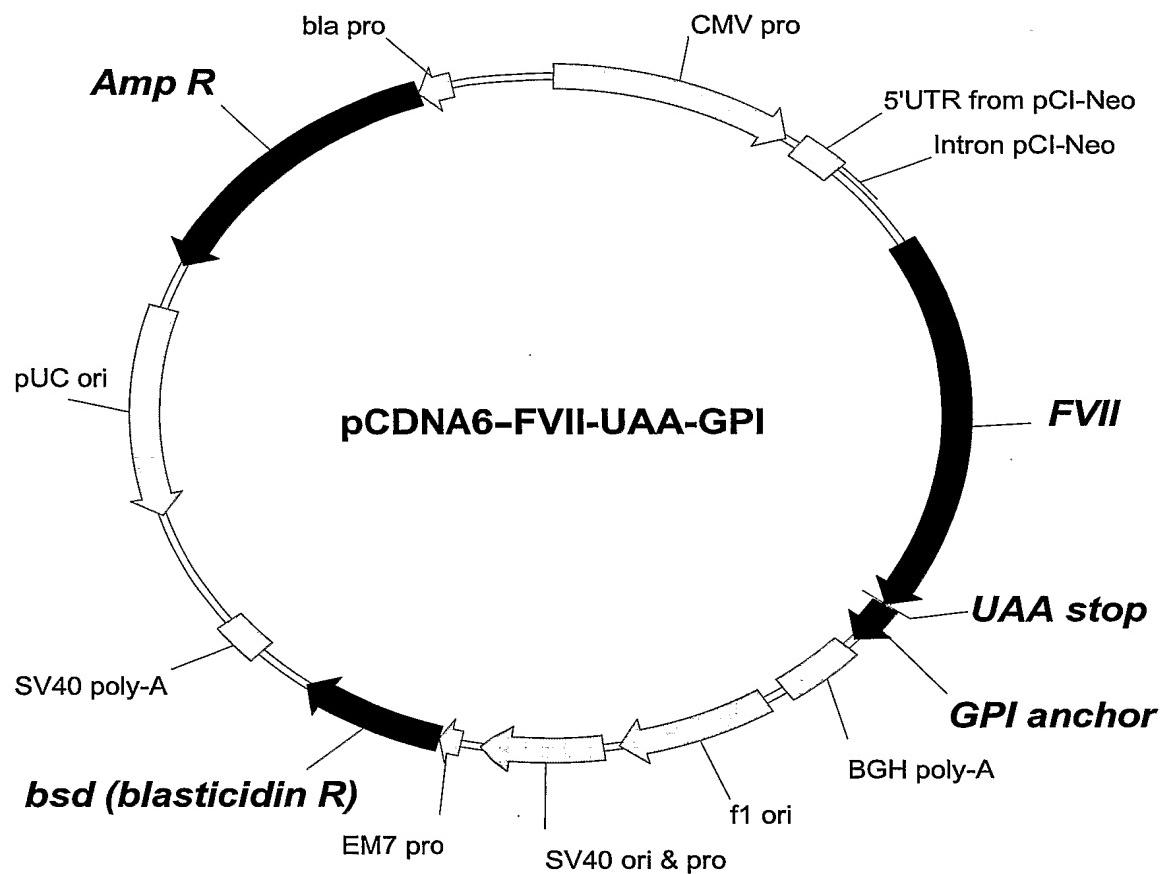
Figure 12

A) Negative CHO-K1 control
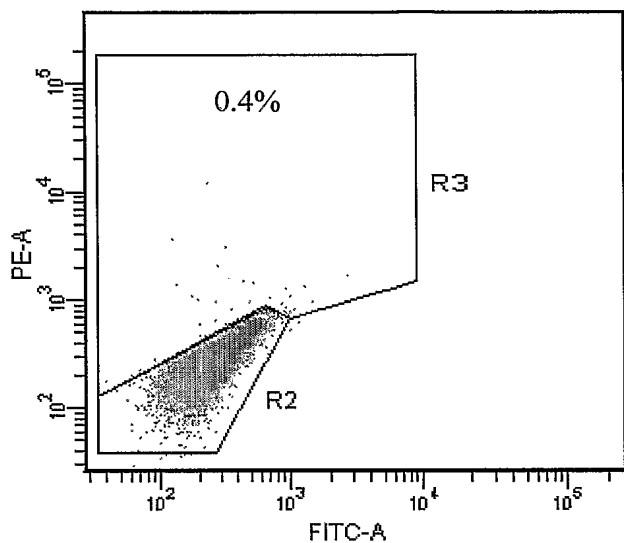
B) Transfected CHO-K1 cells
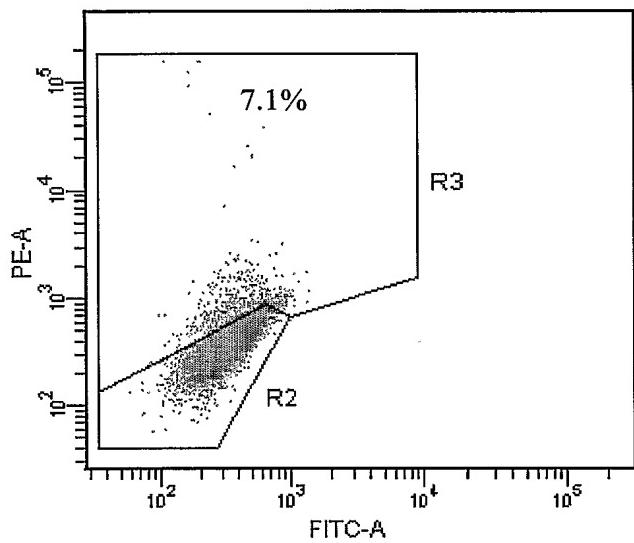
Figure 13

A) Negative CHO-K1 control
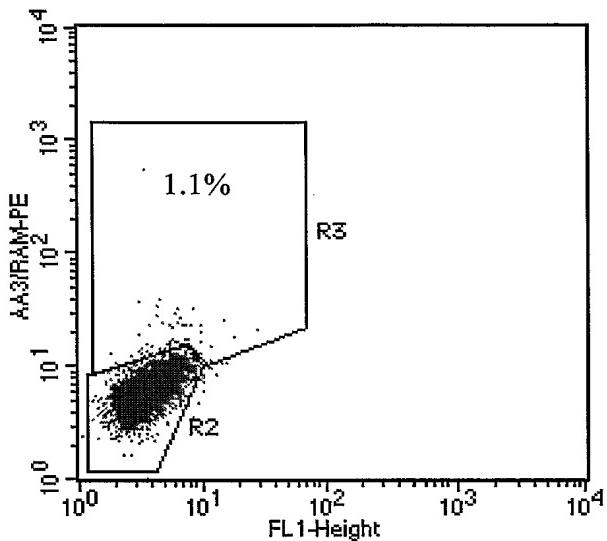
B) Transfected CHO-K1 cells
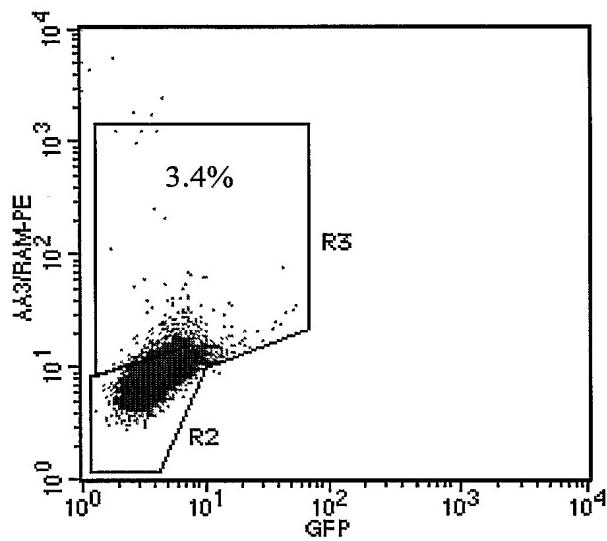
Figure 14 (PC-GPI)

```
          M   W   Q   L   T   S   L     L   L   F   V   A   T   W     G   I   S     G   T   P
   1   ATGTGGCAGC TCACAAGCCT CCTGCTGTTC GTGGCCACCT GGGGAATTTC CGGCACACCA
          A   P   L   D   S   V   F     S   S   S   E   R   A   H     Q   V   L     R   I   R
  61   GCTCCTCTTG ACTCAGTGTT CTCCAGCAGC GAGCGTGCCC ACCAGGTGCT GCGCATCCGC
          K   R   A   N   S   F   L     E   E   L   R   H   S   S     L   E   R     E   C   I
 121   AAACGTGCCA ACTCCTTCCT GGAGGAGCTC CGTCACAGCA GCCTGGAGCG GGAGTGCATA
          E   E   I   C   D   F   E     A   K   E   I   F   Q   N     V   D   D     T   L
 181   GAGGAGATCT GTGACTTCGA GGAGGCCAAG GAAATTTTCC AAAATGTGGA TGACACACTG
          A   F   W   S   K   H   V     D   G   D   Q   C   L   V     L   P   L     E   H   P
 241   GCCTTCTGGT CCAAGCACGT CGACGGTGAC CAGTGCTTGG TCTTGCCCTT GGAGCACCCG
          C   A   S   L   C   C   G     H   G   T   C   I   D   G     I   G   S     F   S   C
 301   TGCGCCAGCC TGTGCTGCGG GCACGGCACG TGCATCGACG GCATCGGCAG CTTCAGCTGC
          D   C   R   S   G   W   E     G   R   F   C   Q   R   E     V   S   F     L   N   C
 361   GACTGCCGCA GCGGCTGGGA GGGCCGCTTC TGCCAGCGCG AGGTGAGCTT CCTCAATTGC
          S   L   D   N   G   G   C     T   H   Y   C   L   E   E     V   G   W     R   R   C
 421   TCGCTGGACA ACGGCGGCTG CACGCATTAC TGCCTAGAGG AGGTGGGCTG GCGGCGCTGT
          S   C   A   P   G   Y   K     L   G   D   D   L   L   Q     C   H   P     A   V   K
 481   AGCTGTGCGC CTGGCTACAA GCTGGGGGAC GACCTCCTGC AGTGTCACCC CGCAGTGAAG
          F   P   C   G   R   P   W     K   R   M   E   K   K   R     S   H   L     K   R   D
 541   TTCCCTTGTG GGAGGCCCTG GAAGCGGATG GAGAAGAAGC GCAGTCACCT GAAACGAGAC
          T   E   D   Q   E   D   Q     V   D   P   R   L   I   D     G   K   M     T   R   R
 601   ACAGAAGACC AAGAAGACCA AGTAGATCCG CGGCTCATTG ATGGGAAGAT GACCAGGCGG
          G   D   S   P   W   Q   V     V   L   L   D   S   K   K     K   L   A     C   G   A
 661   GGAGACAGCC CCTGGCAGGT GGTCCTGCTG GACTCAAAGA AGAAGCTGGC CTGCGGGGCA
          V   L   I   H   P   S   W     V   L   T   A   A   H   C     M   D   E     S   K   K
 721   GTGCTCATCC ACCCCTCCTG GGTGCTGACA GCGGCCCACT GCATGGATGA GTCCAAGAAG
          L   L   V   R   L   G   E     Y   D   L   R   R   W   E     K   W   E     L   D   L
 781   CTCCTTGTCA GGCTTGGAGA GTATGACCTG CGGCGCTGGG AGAAGTGGGA GCTGGACCTG
          D   I   K   E   V   F   V     H   P   N   Y   S   K   S     T   T   D     N   D   I
 841   GACATCAAGG AGGTCTTCGT CCACCCCAAC TACAGCAAGA GCACCACCGA CAATGACATC
          A   L   L   H   L   A   Q     P   A   T   L   S   Q   T     I   V   P     I   C   L
 901   GCACTGCTGC ACCTGGCCCA GCCCGCCACC CTCTCGCAGA CCATAGTGCC CATCTGCCTC
          P   D   S   G   L   A   E     R   E   L   N   Q   A   G     Q   E   T     L   V   T
 961   CCGGACAGCG GCCTTGCAGA GCGCGAGCTC AATCAGGCCG GCCAGGAGAC CCTCGTGACG
          G   W   G   Y   H   S     R   E   K   E   A   K   R     N   R   T     F   V   L
1021   GGCTGGGGAT ATCACAGCAG CCGAGAGAAG GAGGCCAAGA GAAACCGCAC CTTCGTCCTC
          N   F   I   K   I   P   V     V   P   H   N   E   C   S     E   V   M     S   N   M
1081   AACTTCATCA AGATTCCCGT GGTCCCGCAC AATGAGTGCA GCGAGGTCAT GAGCAACATG
          V   S   E   N   M   L   C     A   G   I   L   G   D   R     Q   D   A     C   E   G
1141   GTGTCTGAGA ACATGCTGTG TGCGGGCATC CTCGGGGACC GGCAGGATGC CTGCGAGGGC
          D   S   G   G   P   M   V     A   S   F   H   G   T   W     F   L   V     G   L   V
1201   GACAGTGGGG GGCCCATGGT CGCCTCCTTC CACGGCACCT GGTTCCTGGT GGGCCTGGTG
          S   W   G   E   G   C   G     L   L   H   N   Y   G   V     Y   T   K     V   S   R
1261   AGCTGGGGTG AGGGCTGTGG GCTCCTTCAC AACTACGGCG TTTACACCAA AGTCAGCCGC
          Y   L   D   W   I   H   G     H   I   R   D   K   E   A     P   Q   K     S   W   A
1321   TACCTCGACT GGATTCATGG GCACATCAGA GACAAGGAAG CCCCCCAGAA GAGCTGGGCA
          P   L   E   P   T   Y   C     D   L   A   P   P   A   G     T   T   D     A   A   H
1381   CCTCTGGAAC CCACGTACTG CGACCTCGCC CCTCCCGCTG GCACGACCGA TGCCGCTCAC
          P   G   R   S   V   V   P     A   L   L   P   L   L   A     G   T   L     L   L   L
1441   CCTGGCCGGA GCGTCGTGCC TGCCCTCCTG CCTCTGCTCG CCGGGACCCT CCTGCTCCTG
          E   T   A   T   A   P   *     *
1501   GAAACCGCTA CCGCTCCCTA GTAA
```

Figure 15 (PC-UAAC-GPI)

```
           M   W   Q   L   T   S   L   L   F   V   A   T   W   G   I   S   G   T   P
    1   ATGTGGCAGC TCACAAGCCT CCTGCTGTTC GTGGCCACCT GGGGAATTTC CGGCACACCA
           A   P   L   D   S   V   F   S   S   S   E   R   A   H   Q   V   L   R   I   R
   61   GCTCCTCTTG ACTCAGTGTT CTCCAGCAGC GAGCGTGCCC ACCAGGTGCT GCGCATCCGC
           K   R   A   N   S   F   L   E   E   L   R   H   S   S   L   E   R   E   C   I
  121   AAACGTGCCA ACTCCTTCCT GGAGGAGCTC CGTCACAGCA GCCTGGAGCG GGAGTGCATA
           E   E   I   C   D   F   E   A   K   E   I   F   Q   N   V   D   D   T   L
  181   GAGGAGATCT GTGACTTCGA GGAGGCCAAG GAAATTTTCC AAAATGTGGA TGACACACTG
           A   F   W   S   K   H   V   D   G   D   Q   C   L   V   L   P   L   E   H   P
  241   GCCTTCTGGT CCAAGCACGT CGACGGTGAC CAGTGCTTGG TCTTGCCCTT GGAGCACCCG
           C   A   S   L   C   C   G   H   G   T   C   I   D   G   I   G   S   F   S   C
  301   TGCGCCAGCC TGTGCTGCGG GCACGGCACG TGCATCGACG GCATCGGCAG CTTCAGCTGC
           D   C   R   S   G   W   E   G   R   F   C   Q   R   E   V   S   F   L   N   C
  361   GACTGCCGCA GCGGCTGGGA GGGCCGCTTC TGCCAGCGCG AGGTGAGCTT CCTCAATTGC
           S   L   D   N   G   G   C   T   H   Y   C   L   E   E   V   G   W   R   R   C
  421   TCGCTGGACA ACGGCGGCTG CACGCATTAC TGCCTAGAGG AGGTGGGCTG GCGGCGCTGT
           S   C   A   P   G   Y   K   L   G   D   D   L   L   Q   C   H   P   A   V   K
  481   AGCTGTGCGC CTGGCTACAA GCTGGGGGAC GACCTCCTGC AGTGTCACCC CGCAGTGAAG
           F   P   C   G   R   P   W   K   R   M   E   K   K   R   S   H   L   K   R   D
  541   TTCCCTTGTG GGAGGCCCTG GAAGCGGATG GAGAAGAAGC GCAGTCACCT GAAACGAGAC
           T   E   D   Q   E   D   Q   V   D   P   R   L   I   D   G   K   M   T   R   R
  601   ACAGAAGACC AAGAAGACCA AGTAGATCCG CGGCTCATTG ATGGGAAGAT GACCAGGCGG
           G   D   S   P   W   Q   V   V   L   L   D   S   K   K   L   A   C   G   A
  661   GGAGACAGCC CCTGGCAGGT GGTCCTGCTG GACTCAAAGA AGAAGCTGGC CTGCGGGGCA
           V   L   I   H   P   S   W   V   L   T   A   A   H   C   M   D   E   S   K   K
  721   GTGCTCATCC ACCCCTCCTG GGTGCTGACA GCGGCCCACT GCATGGATGA GTCCAAGAAG
           L   L   V   R   L   G   E   Y   D   L   R   R   W   E   K   W   E   L   D   L
  781   CTCCTTGTCA GGCTTGGAGA GTATGACCTG CGGCGCTGGG AGAAGTGGGA GCTGGACCTG
           D   I   K   E   V   F   V   H   P   N   Y   S   K   S   T   T   D   N   D   I
  841   GACATCAAGG AGGTCTTCGT CCACCCCAAC TACAGCAAGA GCACCACCGA CAATGACATC
           A   L   L   H   L   A   Q   P   A   T   L   S   Q   T   I   V   P   I   C   L
  901   GCACTGCTGC ACCTGGCCCA GCCCGCCACC CTCTCGCAGA CCATAGTGCC CATCTGCCTC
           P   D   S   G   L   A   E   R   E   L   N   Q   A   G   Q   E   T   L   V   T
  961   CCGGACAGCG GCCTTGCAGA GCGCGAGCTC AATCAGGCCG GCCAGGAGAC CCTCGTGACG
           G   W   G   Y   H   S   S   R   E   K   E   A   K   R   N   R   T   F   V   L
 1021   GGCTGGGGAT ATCACAGCAG CCGAGAGAAG GAGGCCAAGA GAAACCGCAC CTTCGTCCTC
           N   F   I   K   I   P   V   V   P   H   N   E   C   S   E   V   M   S   N   M
 1081   AACTTCATCA AGATTCCCGT GGTCCCGCAC AATGAGTGCA GCGAGGTCAT GAGCAACATG
           V   S   E   N   M   L   C   A   G   I   L   G   D   R   Q   D   A   C   E   G
 1141   GTGTCTGAGA ACATGCTGTG TGCGGGCATC CTCGGGGACC GGCAGGATGC CTGCGAGGGC
           D   S   G   G   P   M   V   A   S   F   H   G   T   W   F   L   V   G   L   V
 1201   GACAGTGGGG GGCCCATGGT CGCCTCCTTC CACGGCACCT GGTTCCTGGT GGGCCTGGTG
           S   W   G   E   G   C   G   L   L   H   N   Y   G   V   Y   T   K   V   S   R
 1261   AGCTGGGGTG AGGGCTGTGG GCTCCTTCAC AACTACGGCG TTTACACCAA AGTCAGCCGC
           Y   L   D   W   I   H   G   H   I   R   D   K   E   A   P   Q   K   S   W   A
 1321   TACCTCGACT GGATTCATGG GCACATCAGA GACAAGGAAG CCCCCCAGAA GAGCTGGGCA
           P   *   L   E   P   T   Y   C   D   L   A   P   P   A   G   T   T   D   A   A
 1381   CCTTAACTGG AACCCACGTA CTGCGACCTC GCCCCTCCCG CTGGCACGAC CGATGCCGCT
           H   P   G   R   S   V   V   P   A   L   L   P   L   L   A   G   T   L   L   L
 1441   CACCCTGGCC GGAGCGTCGT GCCTGCCCTC CTGCCTCTGC TCGCCGGGAC CCTCCTGCTC
           L   E   T   A   T   A   P   *   *   *   *
 1501   CTGGAAACCG CTACCGCTCC CTAGTAATAG TGA
```

Figure 16 (PC-UGAC-GPI)

```
        M   W   Q   L   T   S   L   L   F   V   A   T   W   G   I   S   G   T   P
   1  ATGTGGCAGC TCACAAGCCT CCTGCTGTTC GTGGCCACCT GGGGAATTTC CGGCACACCA
        A   P   L   D   S   V   F   S   S   S   E   R   A   H   Q   V   L   R   I   R
  61  GCTCCTCTTG ACTCAGTGTT CTCCAGCAGC GAGCGTGCCC ACCAGGTGCT GCGCATCCGC
        K   R   A   N   S   F   L   E   E   L   R   H   S   S   L   E   R   E   C   I
 121  AAACGTGCCA ACTCCTTCCT GGAGGAGCTC CGTCACAGCA GCCTGGAGCG GGAGTGCATA
        E   E   I   C   D   F   E   A   K   E   I   F   Q   N   V   D   D   T   L
 181  GAGGAGATCT GTGACTTCGA GGAGGCCAAG GAAATTTTCC AAAATGTGGA TGACACACTG
        A   F   W   S   K   H   V   D   G   D   Q   C   L   V   L   P   L   E   H   P
 241  GCCTTCTGGT CCAAGCACGT CGACGGTGAC CAGTGCTTGG TCTTGCCCTT GGAGCACCCG
        C   A   S   L   C   C   G   H   G   T   C   I   D   G   I   G   S   F   S   C
 301  TGCGCCAGCC TGTGCTGCGG GCACGGCACG TGCATCGACG GCATCGGCAG CTTCAGCTGC
        D   C   R   S   G   W   E   G   R   F   C   Q   R   E   V   S   F   L   N   C
 361  GACTGCCGCA GCGGCTGGGA GGGCCGCTTC TGCCAGCGCG AGGTGAGCTT CCTCAATTGC
        S   L   D   N   G   G   C   T   H   Y   C   L   E   E   V   G   W   R   R   C
 421  TCGCTGGACA ACGGCGGCTG CACGCATTAC TGCCTAGAGG AGGTGGGCTG GCGGCGCTGT
        S   C   A   P   G   Y   K   L   G   D   D   L   L   Q   C   H   P   A   V   K
 481  AGCTGTGCGC CTGGCTACAA GCTGGGGGAC GACCTCCTGC AGTGTCACCC CGCAGTGAAG
        F   P   C   G   R   P   W   K   R   M   E   K   K   R   S   H   L   K   R   D
 541  TTCCCTTGTG GGAGGCCCTG GAAGCGGATG GAGAAGAAGC GCAGTCACCT GAAACGAGAC
        T   E   D   Q   E   D   Q   V   D   P   R   L   I   D   G   K   M   T   R   R
 601  ACAGAAGACC AAGAAGACCA AGTAGATCCG CGGCTCATTG ATGGGAAGAT GACCAGGCGG
        G   D   S   P   W   Q   V   V   L   L   D   S   K   K   L   A   C   G   A
 661  GGAGACAGCC CCTGGCAGGT GGTCCTGCTG GACTCAAAGA AGAAGCTGGC CTGCGGGGCA
        V   L   I   H   P   S   W   V   L   T   A   A   H   C   M   D   E   S   K   K
 721  GTGCTCATCC ACCCCTCCTG GGTGCTGACA GCGGCCCACT GCATGGATGA GTCCAAGAAG
        L   L   V   R   L   G   E   Y   D   L   R   R   W   E   K   W   E   L   D   L
 781  CTCCTTGTCA GGCTTGGAGA GTATGACCTG CGGCGCTGGG AGAAGTGGGA GCTGGACCTG
        D   I   K   E   V   F   V   H   P   N   Y   S   K   S   T   T   D   N   D   I
 841  GACATCAAGG AGGTCTTCGT CCACCCCAAC TACAGCAAGA GCACCACCGA CAATGACATC
        A   L   L   H   L   A   Q   P   A   T   L   S   Q   T   I   V   P   I   C   L
 901  GCACTGCTGC ACCTGGCCCA GCCCGCCACC CTCTCGCAGA CCATAGTGCC CATCTGCCTC
        P   D   S   G   L   A   E   R   E   L   N   Q   A   G   Q   E   T   L   V   T
 961  CCGGACAGCG GCCTTGCAGA GCGCGAGCTC AATCAGGCCG GCCAGGAGAC CCTCGTGACG
        G   W   G   Y   H   S   S   R   E   K   E   A   K   R   N   R   T   F   V   L
1021  GGCTGGGGAT ATCACAGCAG CCGAGAGAAG GAGGCCAAGA GAAACCGCAC CTTCGTCCTC
        N   F   I   K   I   P   V   V   P   H   N   E   C   S   E   V   M   S   N   M
1081  AACTTCATCA AGATTCCCGT GGTCCCGCAC AATGAGTGCA GCGAGGTCAT GAGCAACATG
        V   S   E   N   M   L   C   A   G   I   L   G   D   R   Q   D   A   C   E   G
1141  GTGTCTGAGA ACATGCTGTG TGCGGGCATC CTCGGGGACC GGCAGGATGC CTGCGAGGGC
        D   S   G   G   P   M   V   A   S   F   H   G   T   W   F   L   V   G   L   V
1201  GACAGTGGGG GGCCCATGGT CGCCTCCTTC CACGGCACCT GGTTCCTGGT GGGCCTGGTG
        S   W   G   E   G   C   G   L   L   H   N   Y   G   V   Y   T   K   V   S   R
1261  AGCTGGGGTG AGGGCTGTGG GCTCCTTCAC AACTACGGCG TTTACACCAA AGTCAGCCGC
        Y   L   D   W   I   H   G   H   I   R   D   K   E   A   P   Q   K   S   W   A
1321  TACCTCGACT GGATTCATGG GCACATCAGA GACAAGGAAG CCCCCCAGAA GAGCTGGGCA
        P   *   L   E   P   T   Y   C   D   L   A   P   P   A   G   T   T   D   A   A
1381  CCTTGACTGG AACCCACGTA CTGCGACCTC GCCCCTCCCG CTGGCACGAC CGATGCCGCT
        H   P   G   R   S   V   V   P   A   L   L   P   L   L   A   G   T   L   L   L
1441  CACCCTGGCC GGAGCGTCGT GCCTGCCCTC CTGCCTCTGC TCGCCGGGAC CCTCCTGCTC
        L   E   T   A   T   A   P   *   *   *   *
1501  CTGGAAACCG CTACCGCTCC CTAGTAATAG TGA
```

Figure 17 (FVII-UAA-GPI)

```
          M   V   S   Q   A   L   R     L   L   C     L   L   L   G     L   Q   G     C   L   A
  1   ATGGTCAGCC AGGCCCTCCG CCTCCTGTGC CTGCTCCTGG GGCTGCAGGG CTGCCTGGCT
          A   V   F   V   T   Q   E     E   A   H     G   V   L   H     R   R   R     R   A   N
 61   GCCGTCTTCG TCACCCAGGA GGAAGCCCAT GGCGTCCTGC ATCGCCGGCG CCGGGCCAAT
          A   F   L   E   E   L   R     P   G   S     L   E   R   E     C   K   E     E   Q   C
121   GCCTTTCTGG AAGAGCTCCG CCCTGGCTCC CTGGAACGCG AATGCAAAGA GGAACAGTGC
          S   F   E   E   A   R   E     I   F   K     D   A   E   R     T   K   L     F   W   I
181   AGCTTTGAGG AAGCCCGGGA GATTTTCAAA GACGCTGAGC GGACCAAACT GTTTTGGATT
          S   Y   S   D   G   D   Q     C   A   S     S   P   C   Q     N   G   G     S   C   K
241   AGCTATAGCG ATGGCGATCA GTGCGCCTCC AGCCCTTGCC AGAACGGGGG CTCCTGCAAA
          D   Q   L   Q   S   Y   I     C   F   C     L   P   A   F     E   G   R     N   C   E
301   GACCAGCTGC AGAGCTATAT CTGCTTCTGC CTGCCTGCCT TTGAGGGGCG CAATTGCGAA
          T   H   K   D   D   Q   L     I   C   V     N   E   N   G     G   C   E     Q   Y   C
361   ACCCATAAGG ATGACCAGCT GATTTGCGTC AACGAAACG GGGGCTGCGA GCAGTACTGC
          S   D   H   T   G   T   K     R   S   C     R   C   H   E     G   Y   S     L   L   A
421   AGCGATCACA CGGGCACGAA GCGGAGCTGC CGCTGCCACG AAGGCTATAG CCTCCTGGCT
          D   G   V   S   C   T   P     T   V   E     Y   P   C   G     K   I   P     I   L   E
481   GACGGGGTGT CCTGCACGCC CACGGTGGAA TACCCTTGCG GGAAGATTCC CATTCTAGAA
          K   R   N   A   S   K   P     Q   G   R     I   V   G   G     K   V   C     P   K   G
541   AAGCGGAACG CTAGCAAACC CCAGGGCCGG ATCGTCGGCG GGAAGGTCTG CCCTAAGGGG
          E   C   P   W   Q   V   L     L   L   V     N   G   A   Q     L   C   G     G   T   L
601   GAGTGCCCCT GGCAGGTCCT GCTCCTGGTC AACGGGGCCC AGCTGTGCGG CGGGACCCTC
          I   N   T   I   W   V   V     S   A   A     H   C   F   D     K   I   K     N   W   R
661   ATCAATACCA TTTGGGTCGT GTCCGCCGCT CACTGCTTCG ATAAGATTAA GAATTGGCGG
          N   L   I   A   V   L   G     E   H   D     L   S   E   H     D   G   D     E   Q   S
721   AACCTCATCG CTGTGCTCGG CGAACACGAT CTGTCCGAGC ATGACGGGGA CGAACAGTCC
          R   R   V   A   Q   V   I     I   P   S     T   Y   V   P     G   T   T     N   H   D
781   CGCCGGGTGG CTCAGGTCAT CATTCCCTCC ACCTATGTGC CTGGCACGAC CAATCACGAT
          I   A   L   L   R   L   H     Q   P   V     V   L   T   D     H   V   V     P   L   C
841   ATCGCTCTGC TCCGCCTCCA CCAGCCCGTC GTGCTCACCG ATCACGTCGT GCCTCTGTGC
          L   P   E   R   T   F   S     E   R   T     L   A   F   V     R   F   S     L   V   S
901   CTGCCTGAGC GGACCTTTAG CGAACGCACG CTGGCTTTCG TCCGCTTTAG CCTCGTGTCC
          G   W   G   Q   L   L   D     R   G   A     T   A   L   E     L   M   V     L   N   V
961   GGCTGGGGCC AGCTGCTCGA CCGGGGCGCT ACCGCTCTCG AGCTGATGGT GCTCAACGTC
          P   R   L   M   T   Q   D     C   L   Q     Q   S   R   K     V   G   D     S   P   N
1021  CCCCGGCTGA TGACCCAGGA CTGCCTGCAG CAGTCCCGCA AGTGGGGGA CTCCCCCAAT
          I   T   E   Y   M   F   C     A   G   Y     S   D   G   S     K   D   S     C   K   G
1081  ATCACGGAGT ATATGTTTTG CGCTGGCTAT AGCGATGGCT CCAAGGATAG CTGCAAGGGG
          D   S   G   G   P   H   A     T   H   Y     R   G   T   W     Y   L   T     G   I   V
1141  GACTCCGGCG GGCCCCATGC CACGCACTAT CGCGGGACCT GGTACCTCAC CGGGATCGTC
          S   W   G   Q   G   C   A     T   V   G     H   F   G   V     Y   T   R     V   S   Q
1201  AGCTGGGGCC AGGGCTGCGC CACGGTGGGG CACTTTGGCG TCTACACGCG CGTCAGCCAG
          Y   I   E   W   L   Q   K     L   M   R     S   E   P   R     P   G   V     L   L   R
1261  TACATTGAGT GGCTGCAGAA GCTCATGCGG AGCGAACCCC GGCCCGGGGT GCTCCTGCGG
          A   P   F   P   *   L   E     P   T   Y     C   D   L   A     P   P   A     G   T   T
1321  GCCCCTTTCC CT*TAA*CTGGA ACCCACGTAC TGCGACCTCG CCCCTCCCGC TGGCACGACC
          D   A   A   H   P   G   R     S   V   V     P   A   L   L     P   L   L     A   G   T
1381  GATGCCGCTC ACCCTGGCCG GAGCGTCGTG CCTGCCCTCC TGCCTCTGCT CGCCGGGACC
          L   L   L   L   E   T   A     T   A   P     *   *   *   *
1441  CTCCTGCTCC TGGAAACCGC TACCGCTCCC *TAGTAATAGT GA*
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Figure 18 (IFN-UGAG)

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       M   A   L   P   F   A   L     L   M   A     L   V   V   L     S   C   K     S   I   C
   1 ATGGCTTTGC CTTTTGCTTT ACTGATGGCC CTGGTGGTGC TCAGCTGCAA GTCCATATGC
       S   L   G   C   D   L   P     Q   T   H     S   L   G   N     R   R   A     L   I   L
  61 TCTCTAGGCT GTGATCTGCC TCAGACCCAC AGCCTGGGTA ATAGGAGGGC CTTGATACTC
       L   A   Q   M   G   R   I     S   P   F     S   C   L   K     D   R   H     D   F   G
 121 CTGGCACAAA TGGGAAGAAT CTCTCCTTTC TCCTGCCTGA AGGACAGACA TGACTTTGGA
       F   P   Q   E   E   F   D     G   N   Q     F   Q   K   A     Q   A   I     S   V   L
 181 TTCCCCCAGG AGGAGTTTGA TGGCAACCAG TTCCAGAAGG CTCAAGCCAT CTCTGTCCTC
       H   E   M   I   Q   Q   T     F   N   L     F   S   T   K     D   S   S     A   T   W
 241 CATGAGATGA TCCAGCAGAC CTTCAATCTC TTCAGCACAA AGGACTCATC TGCTACTTGG
       E   Q   S   L   L   E   K     F   S   T     E   L   N   Q     Q   L   N     D   L   E
 301 GAACAGAGCC TCCTAGAAAA ATTTTCCACT GAACTTAACC AGCAGCTGAA TGACCTGGAA
       A   C   V   I   Q   E   V     G   V   E     E   T   P   L     M   N   V     D   S   I
 361 GCCTGCGTGA TACAGGAGGT TGGGGTGGAA GAGACTCCCC TGATGAATGT GGACTCCATC
       L   A   V   K   K   Y   F     Q   R   I     T   L   Y   L     T   E   K     K   Y   S
 421 CTGGCTGTGA AGAAATACTT CCAAAGAATC ACTCTTTATC TGACAGAGAA GAAATACAGC
       P   C   A   W   E   V   V     R   A   E     I   M   R   S     F   S   L     S   K   I
 481 CCTTGTGCCT GGGAGGTTGT CAGAGCAGAA ATCATGAGAT CCTTCTCTTT ATCAAAAATT
       F   Q   E   R   L   R   R     K   E   A     A   A   G   A     P   V   P     Y   P   D
 541 TTTCAAGAAA GATTAAGGAG GAAGGAAGCG GCCGCA GGTG CGCCGGTGCC GTATCCGGAC
       P   L   E   P   R   K   E     T   A   A     A   K   F   E     R   Q   H     M   D   S
 601 CCGCTGGAAC CGCGTAAAGA AACCGCTGCT GCTAAATTCG AACGCCAGCA CATGGACAGC
       *   G   K   P   I   P   N     P   L   L     G   L   D   S     T   L   E     P   T   Y
 661 TGAGGTAAGC CTATCCCTAA CCCTCTCCTC GGTCTCGATT CTACGCTGGA ACCCACGTAC
       C   D   L   A   P   P   A     G   T   T     D   A   A   H     P   G   R     S   V   V
 721 TGCGACCTCG CCCCTCCCGC TGGCACGACC GATGCCGCTC ACCCTGGCCG GAGCGTCGTG
       P   A   L   L   P   L   L     A   G   T     L   L   L   L     E   T   A     T   A   P
 781 CCTGCCCTCC TGCCTCTGCT CGCCGGGACC CTCCTGCTCC TGGAAACCGC TACCGCTCCC
       *   *   *   *
 841 TAGTAATAGT GA
```

Figure 19
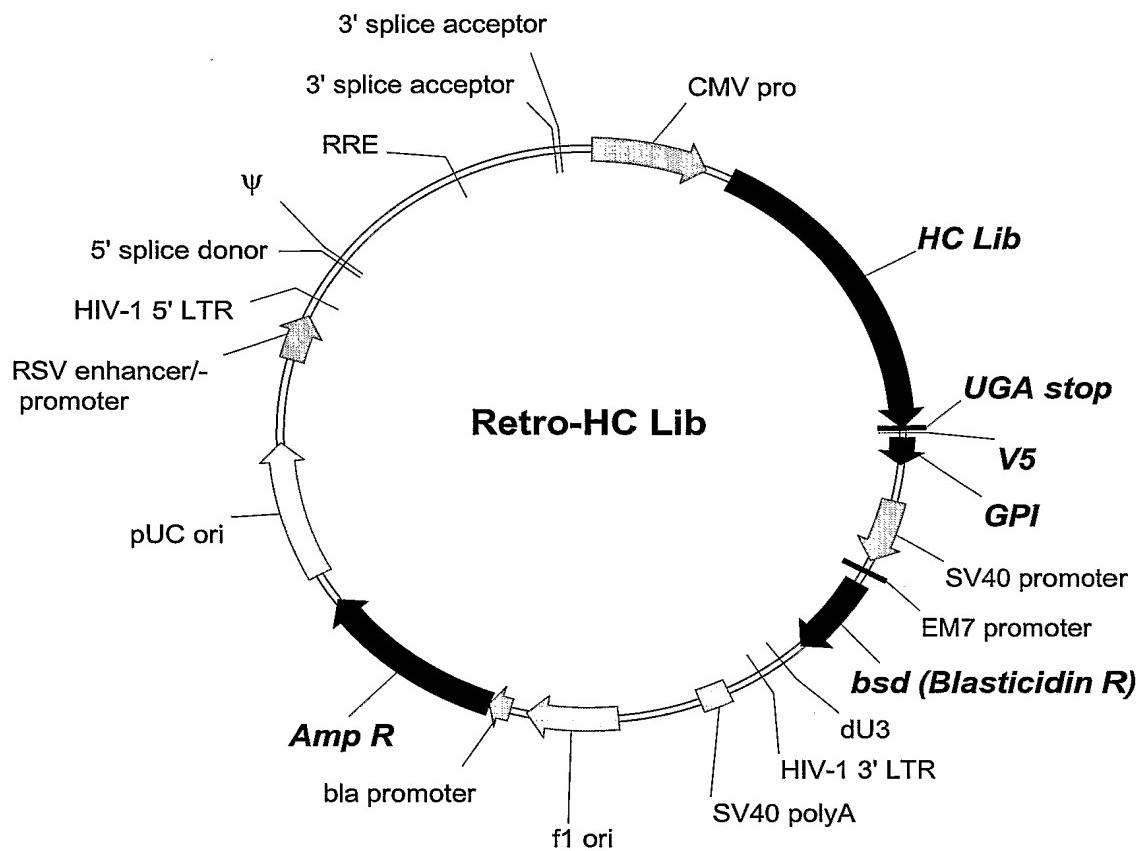
Figure 20
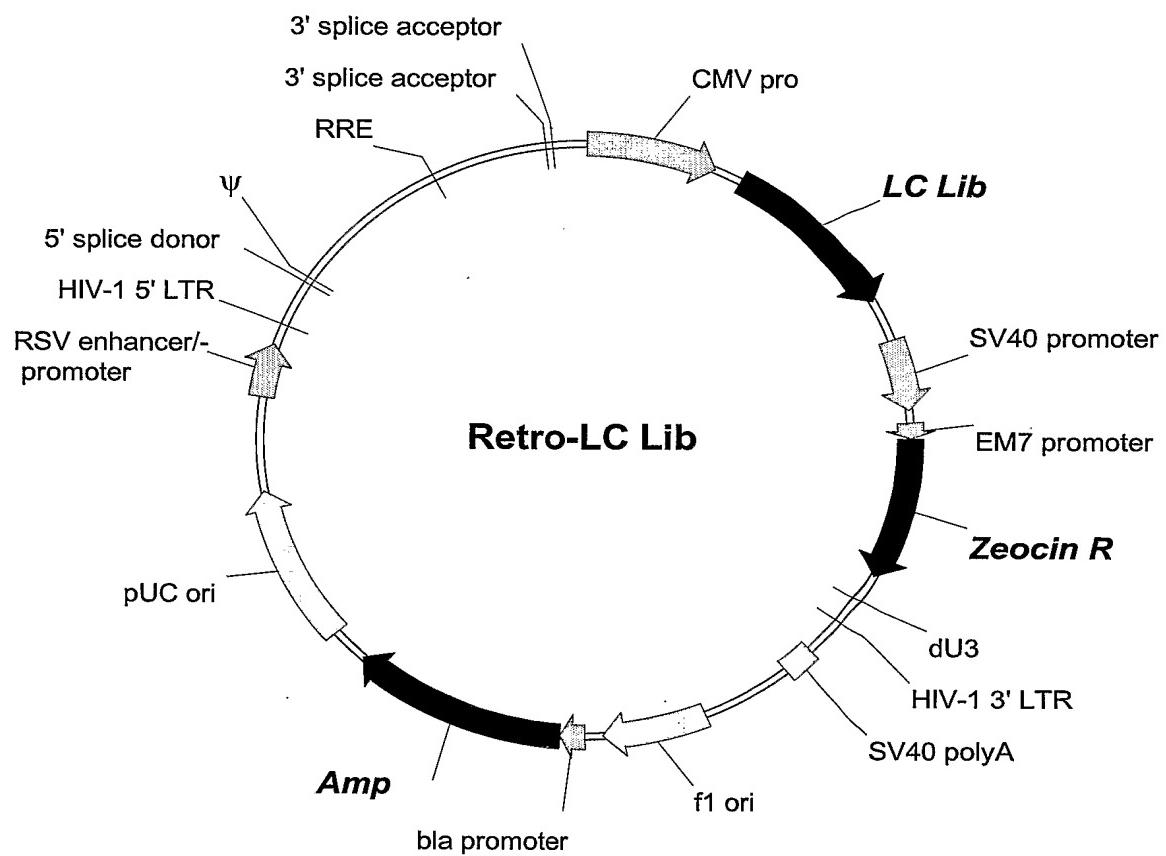
Figure 21
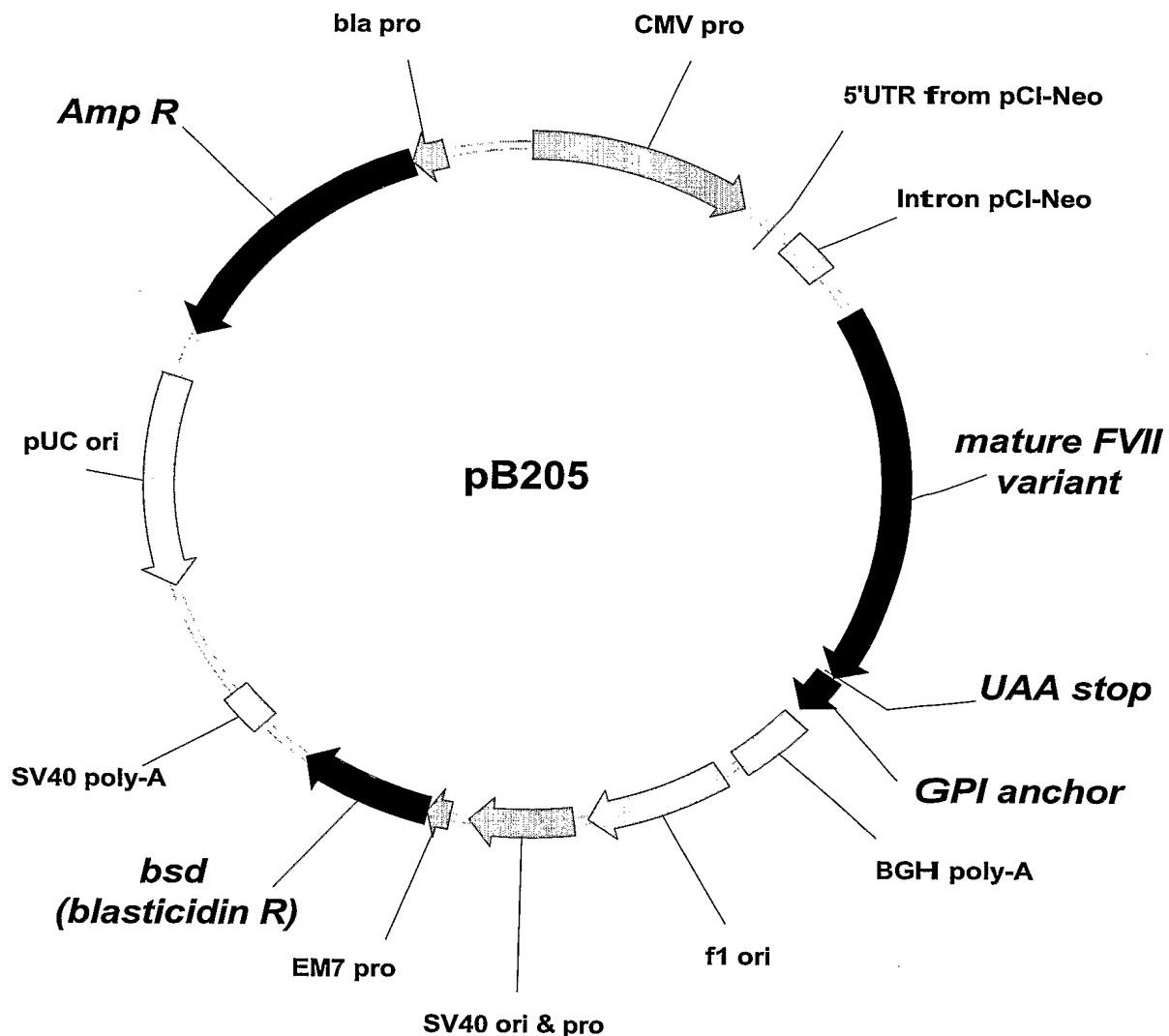
Figure 22 (FVII variant-UAA-GPI)

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        M   V   S   Q     A   L   R     L   L   C     L   L   L   G     L   Q   G     C   L   A
   1  ATGGTCAGCC AGGCCCTCCG CCTCCTGTGC CTGCTCCTGG GGCTGCAGGG CTGCCTGGCT
        A   V   F   V     T   Q   E     E   A   H     G   V   L   H     R   R   R     R   A   N
  61  GCCGTCTTCG TCACCCAGGA GGAAGCCCAT GGCGTCCTGC ATCGCCGGCG CCGGGCCAAT
        A   F   L   E     E   L   R     Q   G   S     L   E   R   E     C   K   E     E   Q   C
 121  GCCTTTCTGG AAGAGCTCCG CCAGGGCTCC CTGGAACGCG AATGCAAAGA GGAACAGTGC
        S   F   E   E     A   R   E     I   F   E     D   E   E   T     K   L     F   W   I
 181  AGCTTTGAGG AAGCCCGCGA GATTTTCGAA GACGAAGAAG AAACCAAGCT GTTTTGGATT
        S   Y   S   D     G   D   Q     C   A   S     S   P   C   Q     N   G   G     S   C   K
 241  AGCTATAGCG ATGGCGATCA GTGCGCCTCC AGCCCTTGCC AGAACGGGGG CTCCTGCAAA
        D   Q   L   Q     S   Y   I     C   F   C     L   P   A   F     E   G   R     N   C   E
 301  GACCAGCTGC AGAGCTATAT CTGCTTCTGC CTGCCTGCCT TTGAGGGGCG CAATTGCGAA
        T   H   K   D     D   Q   L     I   C   V     N   E   N   G     G   C   E     Q   Y   C
 361  ACCCATAAGG ATGACCAGCT GATTTGCGTC AACGAAAACG GGGGCTGCGA GCAGTACTGC
        S   D   H   N     G   T   K     R   S   C     R   C   H   E     G   Y   S     L   L   A
 421  AGCGATCACA ACGGCACGAA GCGGAGCTGC CGCTGCCACG AAGGCTATAG CCTCCTGGCT
        D   G   V   S     C   T   P     T   V   E     Y   P   C   G     K   I   P     I   L   E
 481  GACGGGGTGT CCTGCACGCC CACGGTGGAA TACCCTTGCG GGAAGATTCC CATTCTAGAA
        K   R   N   A     S   K   P     Q   G   R     I   V   G   G     K   V   C     P   K   G
 541  AAGCGGAACG CCAGCAAACC CCAGGGCCGG ATCGTCGGCG GGAAGGTCTG CCCTAAGGGG
        E   C   P   W     Q   V   L     L   L   V     N   G   A   Q     L   C   G     G   T   L
 601  GAGTGCCCCT GGCAGGTCCT GCTCCTGGTC AACGGGCCC AGCTGTGCGG CGGGACCCTC
        I   N   T   I     W   V   V     S   A   A     H   C   F   D     K   I   K     N   W   R
 661  ATCAATACCA TTTGGGTCGT GTCCGCCGCT CACTGCTTCG ATAAGATTAA GAATTGGCGG
        N   L   I   A     V   L   G     E   H   D     L   S   E   H     D   G   D     E   Q   S
 721  AACCTCATCG CTGTGCTCGG CGAACACGAT CTGTCCGAGC ATGACGGGGA CGAACAGTCC
        R   R   V   A     Q   V   I     I   P   S     T   Y   V   P     G   T   T     N   H   D
 781  CGCCGGGTGG CTCAGGTCAT CATTCCCTCC ACCTATGTGC CTGGCACGAC CAATCACGAT
        I   A   L   L     R   L   H     Q   P   V     N   L   T   D     H   V   V     P   L   C
 841  ATCGCTCTGC TCCGCCTCCA CCAGCCCGTC AACCTCACCG ATCACGTCGT GCCTCTGTGC
        L   P   E   R     T   F   S     E   R   T     L   A   F   V     R   F   S     L   V   S
 901  CTGCCTGAGC GGACCTTTAG CGAACGCACG CTGGCTTTCG TCCGCTTTAG CCTCGTGTCC
        G   W   G   Q     L   L   D     R   G   A     T   A   L   E     L   M   V     L   N   V
 961  GGCTGGGGCC AGCTGCTCGA CCGGGGCGCT ACCGCTCTCG AGCTGATGGT GCTCAACGTC
        P   R   L   M     T   Q   D     C   L   Q     Q   S   R   K     V   G   D     S   P   N
1021  CCCCGGCTGA TGACCCAGGA CTGCCTGCAG CAGTCCCGCA AAGTGGGGGA CTCCCCCAAT
        I   T   E   Y     M   F   C     A   G   Y     S   D   G   S     K   D   S     C   K   G
1081  ATCACGGAGT ATATGTTTTG CGCTGGCTAT AGCGATGGCT CCAAGGATAG CTGCAAGGGG
        D   S   G   G     P   H   A     T   H   Y     R   G   T   W     Y   L   T     G   I   V
1141  GACTCCGGCG GGCCCCATGC CACGCACTAT CGCGGGACCT GGTACCTCAC CGGGATCGTC
        S   W   G   Q     G   C   A     T   V   G     H   F   G   V     Y   T   R     V   S   Q
1201  AGCTGGGGCC AGGGCTGCGC CACGGTGGGG CACTTTGGCG TCTACACGCG CGTCAGCCAG
        Y   I   E   W     L   Q   K     L   M   R     S   E   P   R     P   G   V     L   L   R
1261  TACATTGAGT GGCTGCAGAA GCTCATGCGG AGCGAACCCC GGCCCGGGGT GCTCCTGCGG
        A   P   F   P     *   L   E     P   T   Y     C   D   L   A     P   P   A     G   T   T
1321  GCCCCTTTCC CT̲T̲A̲A̲CTGGA ACCCACGTAC TGCGACCTCG CCCCTCCCGC TGGCACGACC
        D   A   A   H     P   G   R     S   V   V     P   A   L   L     P   L   L     A   G   T
1381  GATGCCGCTC ACCCTGGCCG GAGCGTCGTG CCTGCCCTCC TGCCTCTGCT CGCCGGGACC
        L   L   L   L     E   T   A     T   A   P     *   *   *   *
1441    CTCCTGCTCC TGGAAACCGC TACCGCTCCC TAGTAATAGT GA
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Figure 23